and any fees required therefor (including fees for net addition of claims) are hereby authorized to be charged to our Deposit Account No. 19-0036.

Amendments

In the Claims:

Please amend the claims as follows:

Please substitute the following claim 26 for currently pending claim 26:

26. (Four times amended) A method for synthesizing a double stranded nucleic acid molecule comprising

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said templates and which comprises said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or

portions thereof, wherein at least one of said first and second recombination sites comprises one or more mutations that enhance recombination specificity, and wherein said first and second recombination sites are not *lox* sites.

Please substitute the following claim 90 for currently pending claim 90:

90. (Once amended) The method of claim 89, wherein said Int recognition sites are selected from the group consisting of an *att*B site, an *att*P site, an *att*L site, an *att*R site, and portions thereof.

Please substitute the following claim 93 for currently pending claim 93:

93. (Once amended) The method of claim 26, wherein said first or second recombination sites comprise transposase recognition sites of one or more transposons or transposable genetic elements.

Please substitute the following claim 96 for currently pending claim 96:

96. (Once amended) The method of claim 95, wherein said integrons are In2 integrons.

Please enter the following new claims 100-102:

100. (New) A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said templates and which comprises said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises one or more mutations that remove one or more stop codons from said recombination sites.

101. (New) A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said templates and which comprises said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises one or more mutations that avoids hairpin formation in said recombination sites.

102. (New) A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said templates and which comprises said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under

conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-16 or a DNA sequence complementary thereto.

103. (New) The method of claim 100, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

104. (New) The method of claim 101, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

105. (New) The method of claim 102, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

106. (New) The method of claim 100, wherein said first or second recombination sites are selected from the group consisting of *att*B sites, *att*P sites, *att*L sites, *att*R sites, *lox* sites, and portions thereof.

107. (New) The method of claim 101, wherein said first or second recombination sites are selected from the group consisting of *att*B sites, *att*P sites, *att*L sites, *att*R sites, *lox* sites, and portions thereof.

108. (New) The method of claim 102, wherein said first or second recombination sites are selected from the group consisting of *att*B sites, *att*P sites, *att*L sites, *att*R sites, *lox* sites, and portions thereof.

109. (New) The method of claim 100, further comprising amplifying said first and second nucleic acid molecules.

110. (New) The method of claim 101, further comprising amplifying said first and second nucleic acid molecules.

111. (New) The method of claim 102, further comprising amplifying said first and second nucleic acid molecules.

112. (New) The method of claim 100, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

113. (New) The method of claim 101, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

114. (New) The method of claim 102, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

115. (New) The method of claim 100, wherein said first and second recombination sites do not recombine with each other.

116. (New) The method of claim 101, wherein said first and second recombination sites do not recombine with each other.

117. (New) The method of claim 102, wherein said first and second recombination sites do not recombine with each other.